

## **OSIRIS Release Notes Version 2.9.1**

### **Improvements in OSIRIS Version 2.9.1**

Version 2.9.1 is a bug-fix release for version 2.9. Version 2.9 release has a bug that can result in two alleles spaced one nucleotide apart being called as a single allele. Version 2.9 release also has two bugs related to incorrect identification of sigmoidal or crater peaks. These bugs were not present in prior release versions. In addition, v. 2.9.1 contains some optional improvements.

### **Bug fixes**

1. Fixed a bug in which two peaks separated by one base pair and having different allele calls could be considered to be a crater resulting in a single allele call for the two alleles falling between the two peaks. A newly added algorithm improves discrimination between craters and closely spaced allele peaks to ensure accurate crater identification. The new algorithm is only applied after baseline normalization and curve fitting are complete, during cross-channel analysis. The only effect of this change is to prevent the omission of correct allele peaks. See User's Guide for additional details.
2. Fixed a bug in the assessment of crater or sigmoidal peaks that could infrequently result in a small allele being designated as a sigmoidal or crater peak. The corrected algorithm prevents such a misidentification. The corrected algorithm is only applied after baseline normalization and curve fitting are complete, during cross-channel analysis. The only effect of this change is to prevent the omission of correct allele peaks.
3. Fixed a bug in which Osiris identifies a sigmoidal peak as a cross-channel pull-up artifact when an expert would have chosen either the negative or positive side peak as the probable pull-up. The corrected algorithm is only applied after baseline normalization and curve fitting are complete, during cross-channel analysis. The only effect of this change is to prevent the omission of correct allele peaks.

### **New Features**

#### **Improved shoulder allele calling**

1. Improved shoulder peak identification by adding an optional enhanced shoulder-finding algorithm. This algorithm can be disabled by the user by unchecking the box "Apply Enhanced Shoulder-Fitting Algorithm" on the Sample Limits tab of the Lab Settings. The algorithm is enabled (checked) by default. This algorithm is an add-on to the standard curve-fitting process that is the backbone of OSIRIS. It runs after the basic curve-fitting algorithm and is separate from it. Even if enabled, the enhanced algorithm is not used for ILS channels and it is not used during the baseline normalization process, so enabling the algorithm will have no effect on the calculated baseline. The new algorithm builds on the peaks discovered in the standard curve-fitting process by examining adjacent pairs of peaks looking for differences in the raw versus analyzed data to identify missing shoulder peaks.

2. Added optional improvement of identification of sample ILS internal marker peaks. This new algorithm enables OSIRIS to correctly analyze the ILS of samples that previously were not able to be analyzed due to ILS analysis failure. If this new algorithm is enabled by the user (in Lab Settings) and it does not successfully analyze a sample ILS, OSIRIS automatically reverts to previous algorithms. Historically, this is of primary use for RAPID DNA platforms. However, it may prove to be useful for ABI systems as well. The default setting is to not enable the new algorithm. If the new algorithm is not enabled in Lab Settings (Save ILS History to Aid Sample Analysis on the Sample Limits tab), the old algorithm is used. See the OSIRIS User's Guide.